



SEQUENCE LISTING

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<120> Receptor Ligands and Methods of Modulating Receptors

<130> 018781-009530US

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<141> 2003-11-21

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<150> US 60/444,153
<151> 2003-01-30

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<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Homo sapiens

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<223> human G-protein coupled receptor TGR4a (HM74)

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tccagccgga tttccctgtt caacctggca gtagctgact ttctactgtat catctgcctg 240
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<212> PRT

<213> Homo sapiens

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<223> human G-protein coupled receptor TGR4a (HM74)

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Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
20 25 30

Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
35 40 45

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
50 55 60

Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
65 70 75 80

Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly
85 90 95

Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
100 105 110

Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
115 120 125

Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala
130 135 140

Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val
145 150 155 160

His Leu Leu Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val
165 170 175

Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met
180 185 190

Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
195 200 205

Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
210 215 220

Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
225 230 235 240

Val Ile Cys Phe Leu Pro Ser Val Val Arg Ile Arg Ile Phe Trp
245 250 255

Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
260 265 270

Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
275 280 285

Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
290 295 300

Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
305 310 315 320

Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
325 330 335

Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro
340 345 350

Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys
355 360 365

Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys
370 375 380

Cys Ile Glu
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<211> 1092
<212> DNA
<213> Homo sapiens

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<223> human G-protein coupled receptor TGR4b

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tccagccgga tttccctgtt caacctggca gtggctgact ttctactgtat catctgcctg 240
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gtggcggttag acaggttattt ccgggtggtc catccccacc acgcccgtt caagatctcc 420
aatcggacag cagccatcat ctcttcgtt ctgtggggca tcactattgg cctgacagtc 480
cacccctgtt agaagaagat gccgatccag aatggcggtt caaatttgc cagcagctt 540
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gaccggcatg ccaagatcaa gagagccatc accttcatca tgggtggcgtt catcgatcttt 720
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tttcccaact tcttctccac tttgtatcaac cgctgcctcc agaggaagat gacaggtgag 960
ccagataata accgcagcac gagcgtcgag ctcacagggg accccaaacaa aaccagaggc 1020
gctccagagg cgttaatggc caactccgtt gagccatggc gccccttta tctggggccca 1080
acctctcattt aa 1092

<210> 4
<211> 363
<212> PRT
<213> Homo sapiens

<220>
<223> human G-protein coupled receptor TGR4b

<400> 4
Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
1 5 10 15

Asn	Cys	Cys	Val	Phe	Arg	Asp	Asp	Phe	Ile	Val	Lys	Val	Leu	Pro	Pro
			20					25					30		
Val	Leu	Gly	Leu	Glu	Phe	Ile	Phe	Gly	Leu	Leu	Gly	Asn	Gly	Leu	Ala
	35			40					45						
Leu	Trp	Ile	Phe	Cys	Phe	His	Leu	Lys	Ser	Trp	Lys	Ser	Ser	Arg	Ile
	50				55					60					
Phe	Leu	Phe	Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu	Ile	Ile	Cys	Leu
	65				70			75				80			
Pro	Phe	Leu	Met	Asp	Asn	Tyr	Val	Arg	Arg	Trp	Asp	Trp	Lys	Phe	Gly
		85				90				95					
Asp	Ile	Pro	Cys	Arg	Leu	Met	Leu	Phe	Met	Leu	Ala	Met	Asn	Arg	Gln
		100				105					110				
Gly	Ser	Ile	Ile	Phe	Leu	Thr	Val	Val	Ala	Val	Asp	Arg	Tyr	Phe	Arg
	115				120				125						
Val	Val	His	Pro	His	His	Ala	Leu	Asn	Lys	Ile	Ser	Asn	Arg	Thr	Ala
	130				135					140					
Ala	Ile	Ile	Ser	Cys	Leu	Leu	Trp	Gly	Ile	Thr	Ile	Gly	Leu	Thr	Val
	145				150				155				160		
His	Leu	Leu	Lys	Lys	Met	Pro	Ile	Gln	Asn	Gly	Gly	Ala	Asn	Leu	
		165				170				175					
Cys	Ser	Ser	Phe	Ser	Ile	Cys	His	Thr	Phe	Gln	Trp	His	Glu	Ala	Met
		180				185				190					
Phe	Leu	Leu	Glu	Phe	Phe	Leu	Pro	Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser
	195					200				205					
Ala	Arg	Ile	Ile	Trp	Ser	Leu	Arg	Gln	Arg	Gln	Met	Asp	Arg	His	Ala
	210				215				220						
Lys	Ile	Lys	Arg	Ala	Ile	Thr	Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe
	225				230				235				240		
Val	Ile	Cys	Phe	Leu	Pro	Ser	Val	Val	Arg	Ile	Arg	Ile	Phe	Trp	
		245				250				255					
Leu	Leu	His	Thr	Ser	Gly	Thr	Gln	Asn	Cys	Glu	Val	Tyr	Arg	Ser	Val
		260				265				270					
Asp	Leu	Ala	Phe	Phe	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met
		275				280				285					
Leu	Asp	Pro	Val	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Asn	Phe
		290			295				300						
Phe	Ser	Thr	Leu	Ile	Asn	Arg	Cys	Leu	Gln	Arg	Lys	Met	Thr	Gly	Glu
	305				310				315				320		
Pro	Asp	Asn	Asn	Arg	Ser	Thr	Ser	Val	Glu	Leu	Thr	Gly	Asp	Pro	Asn
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Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro
340 345 350

Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Pro
355 360

<210> 5
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<212> DNA
<213> Homo sapiens

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<223> human G-protein coupled receptor TGR183

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tgcctccaca tgaagacactg gaagccccagc actgtttacc tttcaattt ggccgtggct 180
gatttcctcc ttatgatctg cctgcctttt cgacagact attacctcag acgttagacac 240
tgggcttttg gggacattcc ctgcccggatg gggcttca cgttggccat gaacaggggcc 300
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caccacgcgg tgaacactat ctccaccatgg gtggcggctg gcatcgtctg caccctgtgg 420
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aggagttca tcagttgtggc aaatagtttt caaagccagt ctgatggca atgggatccc 1020
cacattgtt agtggcactg a 1041

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<213> Homo sapiens

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Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
20 25 30

Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
35 40 45

Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
50 55 60

Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65 70 75 80

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95

 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
 100 105 110

 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125

 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140

 Leu Gly Thr Val Tyr Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160

 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175

 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 180 185 190

 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 195 200 205

 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
 210 215 220

 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
 225 230 235 240

 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
 245 250 255

 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
 260 265 270

 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
 275 280 285

 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
 290 295 300

 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
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 325 330 335

 Gln Trp Asp Pro His Ile Val Glu Trp His
 340 345

<210> 7
 <211> 1164
 <212> DNA
 <213> Homo sapiens

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 <223> human G-protein coupled receptor TGR4a allele 2

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aattggacag cagccatcat ctcttcgtt ctgtggggca tcactgttgg cctaacagtc 480
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<212> PRT
<213> Homo sapiens

<220>
<223> human G-protein coupled receptor TGR4a allele 2

<400> 8
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Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
20 25 30

Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
35 40 45

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
50 55 60

Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
 65 70 75 80

Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Lys Phe Gly
85 90 95

Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
100 105 110

Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
115 120 125

Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala
130 135 140

Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val
145 150 155 160

His	Leu	Leu	Lys	Lys	Leu	Leu	Ile	Gln	Asn	Gly	Pro	Ala	Asn	Val	
							165		170					175	
Cys	Ile	Ser	Phe	Ser	Ile	Cys	His	Thr	Phe	Arg	Trp	His	Glu	Ala	Met
							180		185					190	
Phe	Leu	Leu	Glu	Phe	Leu	Leu	Pro	Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser
							195		200					205	
Ala	Arg	Ile	Ile	Trp	Ser	Leu	Arg	Gln	Arg	Gln	Met	Asp	Arg	His	Ala
							210		215					220	
Lys	Ile	Lys	Arg	Ala	Ile	Thr	Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe
							225		230					240	
Val	Ile	Cys	Phe	Leu	Pro	Ser	Val	Val	Val	Arg	Ile	Arg	Ile	Phe	Trp
							245		250					255	
Leu	Leu	His	Thr	Ser	Gly	Thr	Gln	Asn	Cys	Glu	Val	Tyr	Arg	Ser	Val
							260		265					270	
Asp	Leu	Ala	Phe	Phe	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met
							275		280					285	
Leu	Asp	Pro	Val	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Asn	Phe
							290		295					300	
Phe	Ser	Thr	Leu	Ile	Asn	Arg	Cys	Leu	Gln	Arg	Lys	Met	Thr	Gly	Glu
							305		310					320	
Pro	Asp	Asn	Asn	Arg	Ser	Thr	Ser	Val	Glu	Leu	Thr	Gly	Asp	Pro	Asn
							325		330					335	
Lys	Thr	Arg	Gly	Ala	Pro	Glu	Ala	Leu	Met	Ala	Asn	Ser	Gly	Glu	Pro
							340		345					350	
Trp	Ser	Pro	Ser	Tyr	Leu	Gly	Pro	Thr	Ser	Asn	Asn	His	Ser	Lys	Lys
							355		360					365	
Gly	His	Cys	His	Gln	Glu	Pro	Ala	Ser	Leu	Glu	Lys	Gln	Leu	Gly	Cys
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Cys	Ile	Glu													
		385													
<210>	9														
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<213>	Artificial Sequence														
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<223>	Description of Artificial Sequence:	poly-Gly													
	flexible linker														
<220>															
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<222>	(6)..(200)														
<223>	Gly residues from position 6 to 200 may be present														
	or absent														

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Gly
35 40 45

Gly
50 55 60

Gly
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Gly
85 90 95

Gly
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Gly
115 120 125

Gly
130 135 140

Gly
145 150 155 160

Gly
165 170 175

Gly
180 185 190

Gly Gly Gly Gly Gly Gly Gly
195 200